

(1) GENERAL INFORMATION:

(i) APPLICANT: Greenspan, Daniel S
Takahara, Kazuhiko
Hoffman, Guy G

(ii) TITLE OF INVENTION: Mammalian Tollod-Like Protein

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Quarles & Brady
(B) STREET: 1 South Pinckney Street
(C) CITY: Madison
(D) STATE: WI
(E) COUNTRY: US
(F) ZIP: 53703

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0,
Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Berson, Bennett J
(B) REGISTRATION NUMBER: 37094
(C) REFERENCE/DOCKET NUMBER: 960296.93839

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 608-251-5000
(B) TELEFAX: 608-251-9166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide probe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACGTCCAGAC CGGAGCGGGT GTGGCCCGAT GGGGTCATCC CGTTTGTGAT TGGAGGGAAT 60
TTCACAGGCA GCCAGAGGGC AGTCTTCCGG CAGGCCATGA GACACTGGGA GAAGCATACC 120
TGTGTACACT TCTTGGAGCG CACAGATGAG GACAGCTATA TTGTATTAC CTACCGACCC 180
TGCGGGTGCT GCTCCTACGT GGGTCGCCGA GGTGGGGGCC CCCAGGCCAT CTCCATCGGC 240
AAGAACTGTG ACAAGTTTGG CATCGTGGTC CATGAGCTGG GCCATGTCAT TGGCTTCTGG 300
CACGAGCACA CGCGGCCCGA CCGCGACCGC 330

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 611..3652
- (D) OTHER INFORMATION: /product= "murine mTll protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACACCCCTT TGCTCTCCGG GCAGTCGGGA GCTTCCCTAG CTTCGGCAGG CTTTAAAGGT 60
CTGGCGGCGT AGAAATGCCT ATCCCCCACC CCCTTCCTCG GTCTCCCTT TCAGTTCAGA 120
TGTGCTGATG TGCAGACCGG ATTCATCTTC CCCGAGCAGC GGCGGTGGCA GCGGCGGGCG 180
CAGGCGGCTG CAGCTCGCTC TCGGCCGCGG GGTCTTGACA GCGGCGGGGG CGCGGCGCGG 240
GAGCCGGAGC TCCGGTGGCA GCTGAGCCCG CCGTGCGCCT CTCGCCGCGG CCGGTCGTGA 300
TCGCGGGAAG TTCGACCGCT GGAAGGACGA CCTAGACCGA GCCGGGTGG C'TGCGGCTGC 360
CCTGCGCCGA GCTCCTCACC TGCCTTCCGC CCACCCGCGG GCGGCGGGCC AAGTTCCCCA 420
GCATCCGGGG GAGACAGGGA GACATTTGCC CTCTCTAGCG TCCTGAAGAC ATCCGCATGT 480
CTCCGGACAC CTGAACATTC AGGTCTTTCC GAGGAGCTTC CCAGTCGGGA TAAGAACACT 540
GTCCCTAGAG CCCCGCATAT CCACGCGGCC CTCCGGGTCT GGTCCCCTCC TTTTCTCTA 600
GGGGAGGAGG ATG GGT TTG CAA GCG CTC TCC CCG AGG ATG CTC CTG TGG 649
Met Gly Leu Gln Ala Leu Ser Pro Arg Met Leu Leu Trp
1 5 10
TTG GTG GTC TCG GGT ATT GTT TTC TCC CGG GTG CTG TGG GTC TGC GCT 697
Leu Val Val Ser Gly Ile Val Phe Ser Arg Val Leu Trp Val Cys Ala
15 20 25
GGC CTC GAT TAT GAT TAC ACT TTT GAT GGG AAC GAA GAG GAC AAA ACG 745
Gly Leu Asp Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr
30 35 40 45
GAG CCT ATA GAT TAC AAG GAC CCG TGC AAA GCT GCT GTG TTT TGG GGT 793
Glu Pro Ile Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly
50 55 60
GAC ATC GCC TTA GAT GAT GAA GAC TTA AAT ATC TTC CAA ATA GAC AGG 841
Asp Ile Ala Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg
65 70 75
ACA ATT GAC CTG ACC CAG AGC CCC TTT GGA AAA CTT GGA CAT ATT ACA 889
Thr Ile Asp Leu Thr Gln Ser Pro Phe Gly Lys Leu Gly His Ile Thr
80 85 90
GGT GGC TTT GGA GAC CAT GGC ATG CCA AAG AAG CGA GGG GCA CTC TAC 937
Gly Gly Phe Gly Asp His Gly Met Pro Lys Lys Arg Gly Ala Leu Tyr
95 100 105

005232 992260

	CAA	CTT	ATA	GAG	AGG	ATC	AGA	AGA	ATT	GGC	TCT	GGC	TTG	GAG	CAA	AAT	985
	Gln	Leu	Ile	Glu	Arg	Ile	Arg	Arg	Ile	Gly	Ser	Gly	Leu	Glu	Gln	Asn	
	110					115				120					125		
5	AAC	ACG	ATG	AAG	GGA	AAA	GCA	CCT	CCA	AAA	TTG	TCA	GAG	CAA	AGT	GAG	1033
	Asn	Thr	Met	Lys	Gly	Lys	Ala	Pro	Pro	Lys	Leu	Ser	Glu	Gln	Ser	Glu	
					130					135					140		
	AAA	AAT	CGA	GTT	CCC	AGA	GCT	GCT	ACC	TCA	AGA	ACG	GAA	AGG	ATA	TGG	1081
	Lys	Asn	Arg	Val	Pro	Arg	Ala	Ala	Thr	Ser	Arg	Thr	Glu	Arg	Ile	Trp	
				145					150					155			
10	CCT	GGG	GGT	GTC	ATT	CCT	TAT	GTC	ATA	GGA	GGA	AAC	TTT	ACT	GGC	AGC	1129
	Pro	Gly	Gly	Val	Ile	Pro	Tyr	Val	Ile	Gly	Gly	Asn	Phe	Thr	Gly	Ser	
				160				165					170				
	CAG	AGA	GCC	ATG	TTC	AAG	CAG	GCC	ATG	AGA	CAC	TGG	GAA	AAG	CAC	ACC	1177
15	Gln	Arg	Ala	Met	Phe	Lys	Gln	Ala	Met	Arg	His	Trp	Glu	Lys	His	Thr	
				175			180					185					
	TGT	GTG	ACG	TTC	ACT	GAG	AGA	AGT	GAT	GAA	GAA	AGT	TAT	ATT	GTG	TTC	1225
	Cys	Val	Thr	Phe	Thr	Glu	Arg	Ser	Asp	Glu	Glu	Ser	Tyr	Ile	Val	Phe	
	190					195				200					205		
20	ACC	TAC	AGG	CCT	TGT	GGA	TGC	TGC	TCC	TAT	GTT	GGT	CGG	CGG	GGA	AAT	1273
	Thr	Tyr	Arg	Pro	Cys	Gly	Cys	Cys	Ser	Tyr	Val	Gly	Arg	Arg	Gly	Asn	
					210					215					220		
	GGC	CCT	CAG	GCC	ATC	TCT	ATT	GGC	AAG	AAC	TGT	GAC	AAG	TTT	GGA	ATT	1321
	Gly	Pro	Gln	Ala	Ile	Ser	Ile	Gly	Lys	Asn	Cys	Asp	Lys	Phe	Gly	Ile	
				225					230					235			
25	GTT	GTT	CAT	GAA	CTG	GGC	CAC	GTG	ATA	GGC	TTC	TGG	CAT	GAA	CAT	ACC	1369
	Val	Val	His	Glu	Leu	Gly	His	Val	Ile	Gly	Phe	Trp	His	Glu	His	Thr	
				240				245					250				
	CGC	CCA	GAC	CGA	GAC	AAC	CAT	GTC	ACC	ATC	ATT	AGA	GAG	AAC	ATC	CAG	1417
	Arg	Pro	Asp	Arg	Asp	Asn	His	Val	Thr	Ile	Ile	Arg	Glu	Asn	Ile	Gln	
				255			260					265					
	CCA	GGT	CAA	GAG	TAC	AAT	TTT	CTA	AAG	ATG	GAG	CCT	GGA	GAA	GTG	AAC	1465
	Pro	Gly	Gln	Glu	Tyr	Asn	Phe	Leu	Lys	Met	Glu	Pro	Gly	Glu	Val	Asn	
				270		275					280				285		
35	TCT	CTT	GGG	GAA	AGA	TAT	GAT	TTT	GAC	AGT	ATC	ATG	CAC	TAC	GCC	AGG	1513
	Ser	Leu	Gly	Glu	Arg	Tyr	Asp	Phe	Asp	Ser	Ile	Met	His	Tyr	Ala	Arg	
					290					295					300		
	AAC	ACC	TTC	TCA	AGA	GGG	ATG	TTT	TTA	GAC	ACA	ATA	CTC	CCC	TCC	CGT	1561
	Asn	Thr	Phe	Ser	Arg	Gly	Met	Phe	Leu	Asp	Thr	Ile	Leu	Pro	Ser	Arg	
				305				310					315				
40	GAT	GAT	AAT	GGC	ATT	CGT	CCT	GCA	ATT	GGT	CAA	CGG	ACC	CGG	TTA	AGC	1609
	Asp	Asp	Asn	Gly	Ile	Arg	Pro	Ala	Ile	Gly	Gln	Arg	Thr	Arg	Leu	Ser	
				320				325					330				
	AAA	GGA	GAC	ATT	GCA	CAA	GCA	AGA	AAG	CTG	TAT	CGA	TGC	CCA	GCA	TGT	1657
45	Lys	Gly	Asp	Ile	Ala	Gln	Ala	Arg	Lys	Leu	Tyr	Arg	Cys	Pro	Ala	Cys	
				335			340					345					
	GGA	GAA	ACC	CTG	CAA	GAA	TCC	AGT	GGC	AAC	CTT	TCT	TCC	CCA	GGA	TTC	1705
	Gly	Glu	Thr	Leu	Gln	Glu	Ser	Ser	Gly	Asn	Leu	Ser	Ser	Pro	Gly	Phe	
				350		355					360				365		
50	CCA	AAT	GGC	TAC	CCT	TCC	TAC	ACA	CAC	TGC	ATC	TGG	AGA	GTG	TCT	GTG	1753
	Pro	Asn	Gly	Tyr	Pro	Ser	Tyr	Thr	His	Cys	Ile	Trp	Arg	Val	Ser	Val	
					370					375					380		

20 25 30

	ACC Thr	CCG Pro	GGG Gly	GAA Glu 385	AAG Lys	ATT Ile	GTC Val	TTG Leu	AAT Asn 390	TTT Phe	ACC Thr	ACA Thr	ATG Met	GAC Asp 395	CTT Leu	TAC Tyr	1801
5	AAA Lys	AGT Ser	AGT Ser 400	TTG Leu	TGC Cys	TGG Trp	TAT Tyr	GAT Asp 405	TAC Tyr	ATT Ile	GAA Glu	GTA Val	AGA Arg 410	GAT Asp	GGT Gly	TAC Tyr	1849
	TGG Trp	AGG Arg 415	AAG Lys	TCA Ser	CCT Pro	CTC Leu	CTT Leu 420	GGT Gly	AGA Arg	TTC Phe	TGT Cys	GGG Gly 425	GAC Asp	AAA Lys	GTG Val	GCT Ala	1897
10	GGA Gly 430	GTT Val	CTT Leu	ACA Thr	TCT Ser	ACG Thr 435	GAC Asp	AGC Ser	AGA Arg	ATG Met	TGG Trp 440	ATT Ile	GAG Glu	TTT Phe	CGT Arg	AGC Ser 445	1945
15	AGC Ser	AGT Ser	AAC Asn	TGG Trp	GTA Val 450	GGA Gly	AAA Lys	GGG Gly	TTT Phe 455	GCA Ala	GCT Ala	GTC Val	TAT Tyr	GAA Glu	GCG Ala 460	ATT Ile	1993
	TGT Cys	GGA Gly	GGG Gly	GAG Glu 465	ATA Ile	AGG Arg	AAA Lys	AAC Asn	GAA Glu 470	GGG Gly	CAG Gln	ATT Ile	CAG Gln	TCT Ser 475	CCC Pro	AAT Asn	2041
20	TAC Tyr	CCC Pro	GAT Asp 480	GAC Asp	TAC Tyr	CGA Arg	CCA Pro	ATG Met 485	AAG Lys	GAG Glu	TGT Cys	GTA Val	TGG Trp 490	AAA Lys	ATA Ile	ATG Met	2089
	GTG Val	TCC Ser 495	GAG Glu	GGC Gly	TAC Tyr	CAT His	GTT Val 500	GGA Gly	CTG Leu	ACC Thr	TTT Phe	CAG Gln 505	GCC Ala	TTT Phe	GAG Glu	ATC Ile	2137
25	GAA Glu 510	AGA Arg	CAT His	GAC Asp	AGC Ser	TGT Cys 515	GCC Ala	TAT Tyr	GAC Asp	CAC His	CTA Leu 520	GAA Glu	GTT Val	CGA Arg	GAT Asp	GGA Gly 525	2185
	GCC Ala	AGT Ser	GAG Glu	AAC Asn	AGC Ser 530	CCT Pro	TTG Leu	ATA Ile	GGA Gly	CGG Arg 535	TTC Phe	TGT Cys	GGT Gly	TAT Tyr	GAC Asp 540	AAA Lys	2233
	CCT Pro	GAA Glu	GAT Asp	ATA Ile 545	AGG Arg	TCT Ser	ACT Thr	TCC Ser	AAC Asn 550	ACC Thr	CTG Leu	TGG Trp	ATG Met	AAG Lys 555	TTT Phe	GTC Val	2281
35	TCT Ser	GAC Asp	GGG Gly 560	ACT Thr	GTG Val	AAC Asn	AAG Lys	GCA Ala 565	GGG Gly	TTT Phe	GCT Ala	GCG Ala	AAC Asn 570	TTT Phe	TTT Phe	AAA Lys	2329
	GAG Glu	GAA Glu 575	GAT Asp	GAG Glu	TGT Cys	GCC Ala 580	AAA Lys	CCT Pro	GAC Asp	CGA Arg	GGA Gly	GGC Gly 585	TGT Cys	GAA Glu	CAG Gln	AGG Arg	2377
40	TGT Cys 590	CTT Leu	AAC Asn	ACA Thr	CTA Leu	GGC Gly 595	AGC Ser	TAC Tyr	CAG Gln	TGT Cys	GCC Ala 600	TGT Cys	GAG Glu	CCT Pro	GGC Gly	TAT Tyr 605	2425
45	GAA Glu	CTG Leu	GGG Gly	CCA Pro	GAC Asp 610	AGA Arg	AGA Arg	AGC Ser	TGT Cys	GAA Glu 615	GCT Ala	GCT Ala	TGC Cys	GGA Gly	GGA Gly 620	CTT Leu	2473
	CTG Leu	ACG Thr	AAG Lys	CTC Leu 625	AAT Asn	GGC Gly	ACC Thr	ATA Ile 630	ACC Thr	CCC Pro	GGC Gly	TGG Trp	CCC Pro 635	AAA Lys	GAG Glu	2521	
50	TAC Tyr	CCT Pro	CCA Pro 640	AAC Asn	AAA Lys	AAC Asn	TGT Cys	GTG Val 645	TGG Trp	CAA Gln	GTG Val	ATC Ile	GCG Ala 650	CCA Pro	AGC Ser	CAG Gln	2569

	TAC Tyr	AGA Arg 655	ATC Ile	TCT Ser	GTG Val	AAG Lys	TTT Phe 660	GAG Glu	TTT Phe	TTT Phe	GAA Glu 665	TTG Leu 665	GAA Glu	GGC Gly	AAT Asn	GAA Glu	2617
5	GTG Val 670	TGC Cys	AAA Lys	TAC Tyr	GAT Asp 675	TAC Tyr	GTG Val	GAG Glu	ATC Ile	TGG Trp	AGC Ser 680	GGC Gly	CCT Pro	TCC Ser	TCT Ser	GAG Glu 685	2665
	TCT Ser	AAA Lys	CTG Leu	CAT His	GGC Gly 690	AAG Lys	TTC Phe	TGT Cys	GGC Gly	GCT Ala 695	GAC Asp	ATA Ile	CCT Pro	GAA Glu	GTG Val 700	ATG Met	2713
10	ACT Thr	TCC Ser	CAT His	TTC Phe 705	AAC Asn	AAC Asn	ATG Met	AGG Arg	ATT Ile 710	GAA Glu	TTC Phe	AAG Lys	TCA Ser	GAC Asp 715	AAC Asn	ACT Thr	2761
15	GTA Val	TCC Ser	AAG Lys 720	AAG Lys	GGC Gly	TTC Phe	AAA Lys	GCA Ala 725	CAT His	TTT Phe	TTC Phe	TCA Ser	GAT Asp 730	AAG Lys	GAT Asp	GAG Glu	2809
	TGT Cys	TCA Ser 735	AAG Lys	GAT Asp	AAT Asn	GGT Gly	GGC Gly 740	TGT Cys	CAG Gln	CAT His	GAG Glu	TGT Cys 745	GTC Val	AAC Asn	ACG Thr	ATG Met	2857
20	GGA Gly 750	AGT Ser	TAC Tyr	ACG Thr	TGT Cys	CAG Gln 755	TGC Cys	CGG Arg	AAT Asn	GGA Gly	TTC Phe 760	GTG Val	TTG Leu	CAT His	GAG Glu	AAC Asn 765	2905
	AAG Lys	CAT His	GAT Asp	TGC Cys	AAG Lys 770	GAA Glu	GCC Ala	GAG Glu	TGT Cys	GAA Glu 775	CAG Gln	AAG Lys	ATA Ile	CAC His	AGC Ser 780	CCA Pro	2953
25	AGT Ser	GGT Gly	CTC Leu	ATC Ile 785	ACC Thr	AGT Ser	CCC Pro	AAC Asn	TGG Trp 790	CCA Pro	GAC Asp	AAG Lys	TAT Tyr	CCA Pro 795	AGC Ser	AGG Arg	3001
30	AAA Lys	GAG Glu	TGC Cys 800	ACG Thr	TGG Trp	GTG Val	ATC Ile 805	AGT Ser	GCC Ala	ATT Ile	CCT Pro	GGC Gly	CAC His 810	CGC Arg	ATC Ile	ACA Thr	3049
	TTA Leu 815	GCC Ala	TTC Phe	AAT Asn	GAG Glu	TTT Phe 820	GAG Glu	GTT Val	GAA Glu	CAA Gln	CAT His	CAA Gln 825	GAA Glu	TGT Cys	GCT Ala	TAT Tyr	3097
35	GAT Asp 830	CAC His	TTG Leu	GAA Glu	ATT Ile 835	TTT Phe	GAT Asp	GGA Gly	GAA Glu	ACG Thr	GAG Glu 840	AAG Lys	TCA Ser	CCA Pro	ATA Ile	CTT Leu 845	3145
	GGC Gly	CGA Arg	CTA Leu	TGT Cys	GGC Gly 850	AGC Ser	AAG Lys	ATA Ile	CCA Pro	GAT Asp 855	CCC Pro	CTC Leu	ATG Met	GCT Ala	ACT Thr 860	GGG Gly	3193
40	AAT Asn	GAA Glu	ATG Met	TTT Phe 865	ATT Ile	CGG Arg	TTT Phe	ATT Ile	TCT Ser 870	GAT Asp	GCC Ala	TCT Ser	GTT Val	CAA Gln 875	AGA Arg	AAA Lys	3241
45	GGC Gly	TTT Phe 880	CAA Gln	GCT Ala	ACA Thr	CAT His	TCC Ser	ACA Thr 885	GAG Glu	TGT Cys	GGT Gly	GGT Gly 890	CGA Arg	TTG Leu	AAA Lys	GCA Ala	3289
	GAG Glu	TCA Ser 895	AAG Lys	CCT Pro	AGA Arg	GAC Asp	CTG Leu 900	TAC Tyr	TCC Ser	CAT His	GCT Ala 905	CAG Gln 905	TTT Phe	GGT Gly	GAT Asp	AAT Asn	3337
50	AAC Asn 910	TAC Tyr	CCA Pro	GGA Gly	CAA Gln 915	CTG Leu	GAC Asp	TGT Cys	GAA Glu	TGG Trp	TTG Leu 920	TTG Leu	GTG Val	TCA Ser	GAA Glu	CGA Arg 925	3385

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Leu Gln Ala Leu Ser Pro Arg Met Leu Leu Trp Leu Val Val
1 5 10 15
Ser Gly Ile Val Phe Ser Arg Val Leu Trp Val Cys Ala Gly Leu Asp
20 25 30
Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Pro Ile
35 40 45
Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala
50 55 60
Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg Thr Ile Asp
65 70 75 80
Leu Thr Gln Ser Pro Phe Gly Lys Leu Gly His Ile Thr Gly Gly Phe
85 90 95
Gly Asp His Gly Met Pro Lys Lys Arg Gly Ala Leu Tyr Gln Leu Ile
100 105 110
Glu Arg Ile Arg Arg Ile Gly Ser Gly Leu Glu Gln Asn Asn Thr Met
115 120 125
Lys Gly Lys Ala Pro Pro Lys Leu Ser Glu Gln Ser Glu Lys Asn Arg
130 135 140
Val Pro Arg Ala Ala Thr Ser Arg Thr Glu Arg Ile Trp Pro Gly Gly
145 150 155 160
Val Ile Pro Tyr Val Ile Gly Gly Asn Phe Thr Gly Ser Gln Arg Ala
165 170 175
Met Phe Lys Gln Ala Met Arg His Trp Glu Lys His Thr Cys Val Thr
180 185 190
Phe Thr Glu Arg Ser Asp Glu Glu Ser Tyr Ile Val Phe Thr Tyr Arg
195 200 205
Pro Cys Gly Cys Cys Ser Tyr Val Gly Arg Arg Gly Asn Gly Pro Gln
210 215 220
Ala Ile Ser Ile Gly Lys Asn Cys Asp Lys Phe Gly Ile Val Val His
225 230 235 240
Glu Leu Gly His Val Ile Gly Phe Trp His Glu His Thr Arg Pro Asp
245 250 255
Arg Asp Asn His Val Thr Ile Ile Arg Glu Asn Ile Gln Pro Gly Gln
260 265 270
Glu Tyr Asn Phe Leu Lys Met Glu Pro Gly Glu Val Asn Ser Leu Gly
275 280 285
Glu Arg Tyr Asp Phe Asp Ser Ile Met His Tyr Ala Arg Asn Thr Phe
290 295 300

Ser 305	Arg	Gly	Met	Phe 310	Leu	Asp	Thr	Ile	Leu	Pro 315	Ser	Arg	Asp	Asp	Asn 320
Gly	Ile	Arg	Pro 325	Ala	Ile	Gly	Gln	Arg	Thr 330	Arg	Leu	Ser	Lys	Gly 335	Asp
Ile	Ala	Gln	Ala 340	Arg	Lys	Leu	Tyr	Arg 345	Cys	Pro	Ala	Cys	Gly 350	Glu	Thr
Leu	Gln	Glu 355	Ser	Ser	Gly	Asn	Leu 360	Ser	Ser	Pro	Gly	Phe 365	Pro	Asn	Gly
Tyr	Pro 370	Ser	Tyr	Thr	His	Cys 375	Ile	Trp	Arg	Val 380	Ser	Val	Thr	Pro	Gly
Glu 385	Lys	Ile	Val	Leu	Asn 390	Phe	Thr	Thr	Met	Asp 395	Leu	Tyr	Lys	Ser	Ser 400
Leu	Cys	Trp	Tyr 405	Asp	Tyr	Ile	Glu	Val 410	Arg	Asp	Gly	Tyr	Trp	Arg 415	Lys
Ser	Pro	Leu 420	Leu	Gly	Arg	Phe	Cys	Gly 425	Asp	Lys	Val	Ala	Gly 430	Val	Leu
Thr	Ser	Thr 435	Asp	Ser	Arg	Met	Trp 440	Ile	Glu	Phe	Arg	Ser 445	Ser	Ser	Asn
Trp	Val 450	Gly	Lys	Gly	Phe	Ala 455	Ala	Val	Tyr	Glu	Ala 460	Ile	Cys	Gly	Gly
Glu 465	Ile	Arg	Lys	Asn 470	Glu	Gly	Gln	Ile	Gln	Ser 475	Pro	Asn	Tyr	Pro	Asp 480
Asp	Tyr	Arg	Pro 485	Met	Lys	Glu	Cys	Val 490	Trp	Lys	Ile	Met	Val	Ser 495	Glu
Gly	Tyr	His 500	Val	Gly	Leu	Thr	Phe	Gln 505	Ala	Phe	Glu	Ile	Glu 510	Arg	His
Asp	Ser	Cys 515	Ala	Tyr	Asp	His	Leu 520	Glu	Val	Arg	Asp	Gly 525	Ala	Ser	Glu
Asn 530	Ser	Pro	Leu	Ile	Gly	Arg 535	Phe	Cys	Gly	Tyr	Asp 540	Lys	Pro	Glu	Asp
Ile 545	Arg	Ser	Thr	Ser	Asn 550	Thr	Leu	Trp	Met	Lys 555	Phe	Val	Ser	Asp	Gly 560
Thr	Val	Asn	Lys 565	Ala	Gly	Phe	Ala	Ala	Asn 570	Phe	Phe	Lys	Glu	Glu 575	Asp
Glu	Cys	Ala	Lys 580	Pro	Asp	Arg	Gly	Gly 585	Cys	Glu	Gln	Arg	Cys	Leu	Asn
Thr	Leu	Gly 595	Ser	Tyr	Gln	Cys	Ala 600	Cys	Glu	Pro	Gly	Tyr 605	Glu	Leu	Gly
Pro 610	Asp	Arg	Arg	Ser	Cys	Glu 615	Ala	Ala	Cys	Gly	Gly 620	Leu	Leu	Thr	Lys
Leu 625	Asn	Gly	Thr	Ile	Thr 630	Thr	Pro	Gly	Trp	Pro 635	Lys	Glu	Tyr	Pro	Pro 640
Asn	Lys	Asn	Cys 645	Val	Trp	Gln	Val	Ile	Ala 650	Pro	Ser	Gln	Tyr	Arg 655	Ile

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	Ser	Val	Lys	Phe	Glu	Phe	Phe	Glu	Leu	Glu	Gly	Asn	Glu	Val	Cys	Lys	
				660					665					670			
	Tyr	Asp	Tyr	Val	Glu	Ile	Trp	Ser	Gly	Pro	Ser	Ser	Glu	Ser	Lys	Leu	
			675					680					685				
5	His	Gly	Lys	Phe	Cys	Gly	Ala	Asp	Ile	Pro	Glu	Val	Met	Thr	Ser	His	
		690					695					700					
	Phe	Asn	Asn	Met	Arg	Ile	Glu	Phe	Lys	Ser	Asp	Asn	Thr	Val	Ser	Lys	
	705					710					715					720	
10	Lys	Gly	Phe	Lys	Ala	His	Phe	Phe	Ser	Asp	Lys	Asp	Glu	Cys	Ser	Lys	
					725					730					735		
	Asp	Asn	Gly	Gly	Cys	Gln	His	Glu	Cys	Val	Asn	Thr	Met	Gly	Ser	Tyr	
				740					745					750			
	Thr	Cys	Gln	Cys	Arg	Asn	Gly	Phe	Val	Leu	His	Glu	Asn	Lys	His	Asp	
			755					760					765				
15	Cys	Lys	Glu	Ala	Glu	Cys	Glu	Gln	Lys	Ile	His	Ser	Pro	Ser	Gly	Leu	
	770						775					780					
	Ile	Thr	Ser	Pro	Asn	Trp	Pro	Asp	Lys	Tyr	Pro	Ser	Arg	Lys	Glu	Cys	
	785					790					795					800	
20	Thr	Trp	Val	Ile	Ser	Ala	Ile	Pro	Gly	His	Arg	Ile	Thr	Leu	Ala	Phe	
					805					810					815		
	Asn	Glu	Phe	Glu	Val	Glu	Gln	His	Gln	Glu	Cys	Ala	Tyr	Asp	His	Leu	
				820					825					830			
	Glu	Ile	Phe	Asp	Gly	Glu	Thr	Glu	Lys	Ser	Pro	Ile	Leu	Gly	Arg	Leu	
				835				840					845				
25	Cys	Gly	Ser	Lys	Ile	Pro	Asp	Pro	Leu	Met	Ala	Thr	Gly	Asn	Glu	Met	
	850						855					860					
	Phe	Ile	Arg	Phe	Ile	Ser	Asp	Ala	Ser	Val	Gln	Arg	Lys	Gly	Phe	Gln	
	865					870					875					880	
30	Ala	Thr	His	Ser	Thr	Glu	Cys	Gly	Gly	Arg	Leu	Lys	Ala	Glu	Ser	Lys	
					885					890					895		
	Pro	Arg	Asp	Leu	Tyr	Ser	His	Ala	Gln	Phe	Gly	Asp	Asn	Asn	Tyr	Pro	
				900					905					910			
	Gly	Gln	Leu	Asp	Cys	Glu	Trp	Leu	Leu	Val	Ser	Glu	Arg	Gly	Ser	Arg	
			915					920					925				
35	Leu	Glu	Leu	Ser	Phe	Gln	Thr	Phe	Glu	Val	Glu	Glu	Glu	Ala	Asp	Cys	
	930						935					940					
	Gly	Tyr	Asp	Tyr	Val	Glu	Val	Phe	Asp	Gly	Leu	Ser	Ser	Lys	Ala	Val	
	945					950					955					960	
40	Gly	Leu	Gly	Arg	Phe	Cys	Gly	Ser	Gly	Pro	Pro	Glu	Glu	Ile	Tyr	Ser	
					965					970					975		
	Ile	Gly	Asp	Val	Ala	Leu	Ile	His	Phe	His	Thr	Asp	Asp	Thr	Ile	Asn	
				980					985					990			
	Lys	Lys	Gly	Phe	Tyr	Ile	Arg	Tyr	Lys	Ser	Ile	Arg	Tyr	Pro	Glu	Thr	
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Met His Ala Lys Asn *
1010

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 648..3689
- (D) OTHER INFORMATION: /product= "human mTll protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CTCACACTTT TGCTCTCTTG CAGTCAGTTG CTTTGCTGGC TTCTGCAGGC TTTTAAGGTC 60
TCGCGGCGTA GAAATGCCTG GCCCCACCC CCTTCCTCGG TCTCCCCTTT CAATTCAGAT 120
GTGCTGATGT GCAGACCGGA TTCATCTTCT CGGAGCTGCG GCGGCGGCTT TGGGCTCAGG 180
CGGCGGCGGC TCGCGCTCGG CCGCGGAGTC CTGGCAGCAG CGGGGACGCG GCGCGGGAGT 240
CCGAGCTCTG GTGGCAGCTG AGCCCGCGGG GCGCCGCTCG CCGAGCCGCG GCCCGGGGAA 300
GTTCCGCAGC CAGAAGGACG ACCTGGCAGG CTGCGAGCGC CAGCGCCGCC AGAGCCGAGT 360
TTGCTGCGC CCTCCCCGCC TCCGAGTGCA GAGTTCCTTA CCTGCCCTCC GCCCACCCGT 420
GGGCCCCTAG CCAACTTCTC CCTGCGACTG GGGGTAACAG GCAGTGCTTG CCCTCTCTAC 480
TGTCCCGGCG GCATCCACAT GTTTCGGAC ACCTGAGCAC CCCGGTCCCG CCGAGGAGCC 540
TCCGGGTGGG GAGAAGAGCA CCGGTGCCCC TAGCCCCGCA CATCAGCGCG GACCGCGGCT 600
GCCTAACCTC TGGGTCCCGT CCCCTCCTTT TCCTCCGGGG GAGGAGG ATG GGG TTG 656
                                         Met Gly Leu
                                         1015
GGA ACG CTT TCC CCG AGG ATG CTC GTG TGG CTG GTG GCC TCG GGG ATT 704
Gly Thr Leu Ser Pro Arg Met Leu Val Trp Leu Val Ala Ser Gly Ile
      1020                      1025                      1030
GTT TTC TAC GGG GAG CTA TGG GTC TGC GCT GGC CTC GAT TAT GAT TAC 752
Val Phe Tyr Gly Glu Leu Trp Val Cys Ala Gly Leu Asp Tyr Asp Tyr
      1035                      1040                      1045
ACT TTT GAT GGG AAC GAA GAG GAT AAA ACA GAG ACT ATA GAT TAC AAG 800
Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Thr Ile Asp Tyr Lys
      1050                      1055                      1060                      1065
GAC CCG TGT AAA GCC GCT GTA TTT TGG GGC GAT ATT GCC TTA GAT GAT 848
Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala Leu Asp Asp
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090236-03290
106226-03290

	GAA GAC TTA AAT ATC TTT CAA ATA GAT AGG ACA ATT GAC CTT ACG CAG	896
	Glu Asp Leu Asn Ile Phe Gln Ile Asp Arg Thr Ile Asp Leu Thr Gln	
	1085 1090 1095	
5	AAC CCC TTT GGA AAC CTT GGA CAT ACC ACA GGT GGA CTT GGA GAC CAT	944
	Asn Pro Phe Gly Asn Leu Gly His Thr Thr Gly Gly Leu Gly Asp His	
	1100 1105 1110	
	GCT ATG TCA AAG AAG CGA GGG GCC CTC TAC CAA CTT ATA GAC AGG ATA	992
	Ala Met Ser Lys Lys Arg Gly Ala Leu Tyr Gln Leu Ile Asp Arg Ile	
	1115 1120 1125	
10	AGA AGA ATT GGC TTT GGC TTG GAG CAA AAC AAC ACA GTT AAG GGA AAA	1040
	Arg Arg Ile Gly Phe Gly Leu Glu Gln Asn Thr Val Lys Gly Lys	
	1130 1135 1140 1145	
15	GTA CCT CTA CAA TTC TCA GGG CAA AAT GAG AAA AAT CGA GTT CCC AGA	1088
	Val Pro Leu Gln Phe Ser Gly Gln Asn Glu Lys Asn Arg Val Pro Arg	
	1150 1155 1160	
	GCC GCT ACA TCA AGA ACG GAA AGA ATA TGG CCT GGA GGC GTT ATT CCT	1136
	Ala Ala Thr Ser Arg Thr Glu Arg Ile Trp Pro Gly Gly Val Ile Pro	
	1165 1170 1175	
20	TAT GTT ATA GGA GGA AAC TTC ACT GGC AGC CAG AGA GCC ATG TTC AAG	1184
	Tyr Val Ile Gly Gly Asn Phe Thr Gly Ser Gln Arg Ala Met Phe Lys	
	1180 1185 1190	
	CAG GCC ATG AGG CAC TGG GAA AAG CAC ACA TGT GTG ACT TTC ATA GAA	1232
	Gln Ala Met Arg His Trp Glu Lys His Thr Cys Val Thr Phe Ile Glu	
	1195 1200 1205	
25	AGA AGT GAT GAA GAG AGT TAC ATT GTA TTC ACC TAT AGG CCT TGT GGA	1280
	Arg Ser Asp Glu Glu Ser Tyr Ile Val Phe Thr Tyr Arg Pro Cys Gly	
	1210 1215 1220 1225	
	TGC TGC TCC TAT GTA GGT CGG CGA GGA AAT GGA CCT CAG GCA ATC TCT	1328
	Cys Cys Ser Tyr Val Gly Arg Arg Gly Asn Gly Pro Gln Ala Ile Ser	
	1230 1235 1240	
	ATC GGC AAG AAC TGT GAT AAA TTT GGG ATT GTT GTT CAT GAA TTG GGT	1376
	Ile Gly Lys Asn Cys Asp Lys Phe Gly Ile Val Val His Glu Leu Gly	
	1245 1250 1255	
35	CAT GTG ATA GGC TTT TGG CAT GAA CAC ACA AGA CCA GAT CGA GAT AAC	1424
	His Val Ile Gly Phe Trp His Glu His Thr Arg Pro Asp Arg Asp Asn	
	1260 1265 1270	
	CAC GTA ACT ATC ATA AGA GAA AAC ATC CAG CCA GGT CAA GAG TAC AAT	1472
	His Val Thr Ile Ile Arg Glu Asn Ile Gln Pro Gly Gln Glu Tyr Asn	
	1275 1280 1285	
40	TTT CTG AAG ATG GAG CCT GGA GAA GTA AAC TCA CTT GGA GAA AGA TAT	1520
	Phe Leu Lys Met Glu Pro Gly Glu Val Asn Ser Leu Gly Glu Arg Tyr	
	1290 1295 1300 1305	
45	GAT TTC GAC AGT ATC ATG CAC TAT GCC AGG AAC ACC TTC TCA AGG GGG	1568
	Asp Phe Asp Ser Ile Met His Tyr Ala Arg Asn Thr Phe Ser Arg Gly	
	1310 1315 1320	
	ATG TTT CTG GAT ACC ATT CTC CCC TCC CGT GAT GAT AAT GGC ATA CGT	1616
	Met Phe Leu Asp Thr Ile Leu Pro Ser Arg Asp Asp Asn Gly Ile Arg	
	1325 1330 1335	
50	CCT GCA ATT GGT CAG CGA ACC CGT CTA AGC AAA GGA GAT ATC GCA CAG	1664
	Pro Ala Ile Gly Gln Arg Thr Arg Leu Ser Lys Gly Asp Ile Ala Gln	
	1340 1345 1350	

004436-0050
T05220-99E4650

	GCA AGA AAG CTG TAT AGA TGT CCA GCA TGT GGA GAA ACT CTA CAA GAA	1712
	Ala Arg Lys Leu Tyr Arg Cys Pro Ala Cys Gly Glu Thr Leu Gln Glu	
	1355 1360 1365	
5	TCC AAT GGC AAC CTT TCC TCT CCA GGA TTT CCC AAT GGC TAC CCT TCT	1760
	Ser Asn Gly Asn Leu Ser Ser Pro Gly Phe Pro Asn Gly Tyr Pro Ser	
	1370 1375 1380 1385	
	TAC ACA CAC TGC ATC TGG AGA GTT TCT GTG ACC CCA GGG GAG AAG ATT	1808
	Tyr Thr His Cys Ile Trp Arg Val Ser Val Thr Pro Gly Glu Lys Ile	
	1390 1395 1400	
10	GTT TTA AAT TTT ACA ACG ATG GAT CTA TAC AAG AGT AGT TTG TGC TGG	1856
	Val Leu Asn Phe Thr Thr Met Asp Leu Tyr Lys Ser Ser Leu Cys Trp	
	1405 1410 1415	
	TAT GAC TAT ATT GAA GTA AGA GAC GGG TAC TGG AGA AAA TCA CCT CTC	1904
	Tyr Asp Tyr Ile Glu Val Arg Asp Gly Tyr Trp Arg Lys Ser Pro Leu	
	1420 1425 1430	
15	CTT GGT AGA TTC TGT GGG GAC AAA TTG CCT GAA GTT CTT ACT TCT ACA	1952
	Leu Gly Arg Phe Cys Gly Asp Lys Leu Pro Glu Val Leu Thr Ser Thr	
	1435 1440 1445	
20	GAC AGC AGA ATG TGG ATT GAG TTT CGT AGC AGC AGT AAT TGG GTA GGA	2000
	Asp Ser Arg Met Trp Ile Glu Phe Arg Ser Ser Ser Asn Trp Val Gly	
	1450 1455 1460 1465	
	AAA GGC TTT GCA GCT GTC TAT GAA GCG ATC TGT GGA GGT GAG ATA CGT	2048
	Lys Gly Phe Ala Ala Val Tyr Glu Ala Ile Cys Gly Gly Glu Ile Arg	
	1470 1475 1480	
25	AAA AAT GAA GGA CAG ATT CAG TCT CCC AAT TAT CCT GAT GAC TAT CGC	2096
	Lys Asn Glu Gly Gln Ile Gln Ser Pro Asn Tyr Pro Asp Asp Tyr Arg	
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	CCG ATG AAA GAA TGT GTG TGG AAA ATA ACA GTG TCT GAG AGC TAC CAC	2144
	Pro Met Lys Glu Cys Val Trp Lys Ile Thr Val Ser Glu Ser Tyr His	
	1500 1505 1510	
	GTC GGG CTG ACC TTT CAG TCC TTT GAG ATT GAA AGA CAT GAC AAT TGT	2192
	Val Gly Leu Thr Phe Gln Ser Phe Glu Ile Glu Arg His Asp Asn Cys	
	1515 1520 1525	
35	GCT TAT GAC TAC CTG GAA GTT AGA GAT GGA ACC AGT GAA AAT AGC CCT	2240
	Ala Tyr Asp Tyr Leu Glu Val Arg Asp Gly Thr Ser Glu Asn Ser Pro	
	1530 1535 1540 1545	
	TTG ATA GGG CGT TTC TGT GGT TAT GAC AAA CCT GAA GAC ATA AGA TCT	2288
	Leu Ile Gly Arg Phe Cys Gly Tyr Asp Lys Pro Glu Asp Ile Arg Ser	
	1550 1555 1560	
40	ACC TCC AAT ACT TTG TGG ATG AAG TTT GTT TCT GAC GGA ACT GTG AAC	2336
	Thr Ser Asn Thr Leu Trp Met Lys Phe Val Ser Asp Gly Thr Val Asn	
	1565 1570 1575	
45	AAA GCA GGG TTT GCT GCT AAC TTT TTT AAA GAG GAA GAT GAG TGT GCC	2384
	Lys Ala Gly Phe Ala Ala Asn Phe Phe Lys Glu Glu Asp Glu Cys Ala	
	1580 1585 1590	
	AAA CCT GAC CGT GGA GGC TGT GAG CAG CGA TGT CTG AAC ACT CTG GGC	2432
	Lys Pro Asp Arg Gly Gly Cys Glu Gln Arg Cys Leu Asn Thr Leu Gly	
	1595 1600 1605	
50	AGT TAC CAG TGT GCC TGT GAG CCT GGC TAT GAG CTG GGC CCA GAC AGA	2480
	Ser Tyr Gln Cys Ala Cys Glu Pro Gly Tyr Glu Leu Gly Pro Asp Arg	
	1610 1615 1620 1625	

0992366
T62307

	AGG	AGC	TGT	GAA	GCT	GCT	TGT	GGT	GGA	CTT	CTT	ACC	AAA	CTT	AAC	GGC	2528
	Arg	Ser	Cys	Glu	Ala	Ala	Cys	Gly	Gly	Leu	Leu	Thr	Lys	Leu	Asn	Gly	
					1630					1635					1640		
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	Thr	Ile	Thr	Thr	Pro	Gly	Trp	Pro	Lys	Glu	Tyr	Pro	Pro	Asn	Lys	Asn	
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	Cys	Val	Trp	Gln	Val	Val	Ala	Pro	Thr	Gln	Tyr	Arg	Ile	Ser	Val	Lys	
					1660				1665					1670			
10	TTT	GAG	TTT	TTT	GAA	TTG	GAA	GGC	AAT	GAA	GTT	TGC	AAA	TAT	GAT	TAT	2672
	Phe	Glu	Phe	Phe	Glu	Leu	Glu	Gly	Asn	Glu	Val	Cys	Lys	Tyr	Asp	Tyr	
		1675					1680						1685				
	GTG	GAG	ATC	TGG	AGT	GGT	CTT	TCC	TCT	GAG	TCT	AAA	CTG	CAT	GGC	AAA	2720
15	Val	Glu	Ile	Trp	Ser	Gly	Leu	Ser	Ser	Glu	Ser	Lys	Leu	His	Gly	Lys	
		1690				1695					1700					1705	
	TTC	TGT	GGC	GCT	GAA	GTG	CCT	GAA	GTG	ATC	ACA	TCC	CAG	TTC	AAC	AAT	2768
	Phe	Cys	Gly	Ala	Glu	Val	Pro	Glu	Val	Ile	Thr	Ser	Gln	Phe	Asn	Asn	
					1710					1715					1720		
	ATG	AGA	ATT	GAA	TTC	AAA	TCT	GAC	AAT	ACT	GTA	TCC	AAG	AAG	GGC	TTC	2816
	Met	Arg	Ile	Glu	Phe	Lys	Ser	Asp	Asn	Thr	Val	Ser	Lys	Lys	Gly	Phe	
					1725				1730					1735			
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	Lys	Ala	His	Phe	Phe	Ser	Asp	Lys	Asp	Glu	Cys	Ser	Lys	Asp	Asn	Gly	
					1740			1745					1750				
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	Gly	Cys	Gln	His	Glu	Cys	Val	Asn	Thr	Met	Gly	Ser	Tyr	Met	Cys	Gln	
		1755					1760					1765					
	TGC	CGT	AAT	GGA	TTT	GTG	CTA	CAT	GAC	AAT	AAA	CAT	GAT	TGC	AAG	GAA	2960
	Cys	Arg	Asn	Gly	Phe	Val	Leu	His	Asp	Asn	Lys	His	Asp	Cys	Lys	Glu	
		1770				1775					1780					1785	
	GCT	GAG	TGT	GAA	CAG	AAG	ATC	CAC	AGT	CCA	AGT	GGC	CTC	ATC	ACC	AGT	3008
	Ala	Glu	Cys	Glu	Gln	Lys	Ile	His	Ser	Pro	Ser	Gly	Leu	Ile	Thr	Ser	
					1790					1795					1800		
35	CCC	AAC	TGG	CCA	GAC	AAG	TAC	CCA	AGC	AGG	AAA	GAA	TGC	ACT	TGG	GAA	3056
	Pro	Asn	Trp	Pro	Asp	Lys	Tyr	Pro	Ser	Arg	Lys	Glu	Cys	Thr	Trp	Glu	
					1805				1810					1815			
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	Ile	Ser	Ala	Thr	Pro	Gly	His	Arg	Ile	Lys	Leu	Ala	Phe	Ser	Glu	Phe	
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	Glu	Ile	Glu	Gln	His	Gln	Glu	Cys	Ala	Tyr	Asp	His	Leu	Glu	Val	Phe	
		1835					1840					1845					
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45	Asp	Gly	Glu	Thr	Glu	Lys	Ser	Pro	Ile	Leu	Gly	Arg	Leu	Cys	Gly	Asn	
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	AAG	ATA	CCA	GAT	CCC	CTT	GTG	GCT	ACT	GGA	AAT	AAA	ATG	TTT	GTT	CGG	3248
	Lys	Ile	Pro	Asp	Pro	Leu	Val	Ala	Thr	Gly	Asn	Lys	Met	Phe	Val	Arg	
					1870				1875					1880			
50	TTT	GTT	TCT	GAT	GCA	TCT	GTT	CAA	AGA	AAA	GGC	TTT	CAA	GCC	ACA	CAT	3296
	Phe	Val	Ser	Asp	Ala	Ser	Val	Gln	Arg	Lys	Gly	Phe	Gln	Ala	Thr	His	
				1885					1890					1895			

TCT ACA GAG TGT GGC GGA CGA TTG AAA GCA GAA TCA AAA CCA AGA GAT 3344
 Ser Thr Glu Cys Gly Gly Arg Leu Lys Ala Glu Ser Lys Pro Arg Asp
 1900 1905 1910

CTG TAC TCA CAT GCT CAG TTT GGT GAT AAC AAC TAC CCA GGA CAG GTT 3392
 Leu Tyr Ser His Ala Gln Phe Gly Asp Asn Asn Tyr Pro Gly Gln Val
 1915 1920 1925

GAC TGT GAA TGG CTA TTA GTA TCA GAA CGG GGC TCT CGA CTT GAA TTA 3440
 Asp Cys Glu Trp Leu Leu Val Ser Glu Arg Gly Ser Arg Leu Glu Leu
 1930 1935 1940 1945

TCC TTC CAG ACA TTT GAA GTG GAG GAA GAA GCA GAC TGT GGC TAT GAC 3488
 Ser Phe Gln Thr Phe Glu Val Glu Glu Glu Ala Asp Cys Gly Tyr Asp
 1950 1955 1960

TAT GTG GAG CTC TTT GAT GGT CTT GAT TCA ACA GCT GTG GGG CTT GGT 3536
 Tyr Val Glu Leu Phe Asp Gly Leu Asp Ser Thr Ala Val Gly Leu Gly
 1965 1970 1975

CGA TTC TGT GGA TCC GGG CCA CCA GAA GAG ATT TAT TCA ATT GGA GAT 3584
 Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu Ile Tyr Ser Ile Gly Asp
 1980 1985 1990

TCA GTT TTA ATT CAT TTC CAC ACT GAT GAC ACA ATC AAC AAG AAG GGA 3632
 Ser Val Leu Ile His Phe His Thr Asp Asp Thr Ile Asn Lys Lys Gly
 1995 2000 2005

TTT CAT ATA AGA TAC AAA AGC ATA AGA TAT CCA GAT ACC ACA CAT ACC 3680
 Phe His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr Thr His Thr
 2010 2015 2020 2025

AAA AAA TAA CACCAAAACC TCTGTCAGAA CACAAAGGAA TGTGCATAAT 3729
 Lys Lys *

GGAGAGAAGA CATATTTTTT TTAAAACTGA AGATATTGGC ACAAATGTTT TATACAAAGA 3789

GTTTGAACAA AAAATCCCTG TAAGACCAGA ATTATCTTTG TACTAAAAGA GAAGTTTCCA 3849

GCAAAACCCCT CATCAGCATT ACAAGGATAT TTGAACTCCA TGCTTGATGG TATTAATAAA 3909

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gly Leu Gly Thr Leu Ser Pro Arg Met Leu Val Trp Leu Val Ala
 1 5 10 15

Ser Gly Ile Val Phe Tyr Gly Glu Leu Trp Val Cys Ala Gly Leu Asp
 20 25 30

Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp Lys Thr Glu Thr Ile
 35 40 45

Asp Tyr Lys Asp Pro Cys Lys Ala Ala Val Phe Trp Gly Asp Ile Ala
 50 55 60

Leu 65	Asp	Asp	Glu	Asp	Leu 70	Asn	Ile	Phe	Gln	Ile 75	Asp	Arg	Thr	Ile	Asp 80
Leu	Thr	Gln	Asn	Pro 85	Phe	Gly	Asn	Leu	Gly 90	His	Thr	Thr	Gly	Gly 95	Leu
Gly	Asp	His	Ala 100	Met	Ser	Lys	Lys	Arg 105	Gly	Ala	Leu	Tyr	Gln 110	Leu	Ile
Asp	Arg	Ile 115	Arg	Arg	Ile	Gly	Phe 120	Gly	Leu	Glu	Gln	Asn 125	Asn	Thr	Val
Lys	Gly 130	Lys	Val	Pro	Leu	Gln 135	Phe	Ser	Gly	Gln	Asn 140	Glu	Lys	Asn	Arg
Val 145	Pro	Arg	Ala	Ala	Thr 150	Ser	Arg	Thr	Glu	Arg 155	Ile	Trp	Pro	Gly	Gly 160
Val	Ile	Pro	Tyr	Val 165	Ile	Gly	Gly	Asn	Phe 170	Thr	Gly	Ser	Gln	Arg 175	Ala
Met	Phe	Lys	Gln 180	Ala	Met	Arg	His	Trp 185	Glu	Lys	His	Thr	Cys 190	Val	Thr
Phe	Ile	Glu 195	Arg	Ser	Asp	Glu	Glu 200	Ser	Tyr	Ile	Val	Phe 205	Thr	Tyr	Arg
Pro	Cys 210	Gly	Cys	Cys	Ser	Tyr 215	Val	Gly	Arg	Arg	Gly 220	Asn	Gly	Pro	Gln
Ala 225	Ile	Ser	Ile	Gly	Lys 230	Asn	Cys	Asp	Lys	Phe 235	Gly	Ile	Val	Val	His 240
Glu	Leu	Gly	His	Val 245	Ile	Gly	Phe	Trp	His 250	Glu	His	Thr	Arg	Pro 255	Asp
Arg	Asp	Asn	His 260	Val	Thr	Ile	Ile	Arg 265	Glu	Asn	Ile	Gln	Pro 270	Gly	Gln
Glu	Tyr	Asn 275	Phe	Leu	Lys	Met	Glu 280	Pro	Gly	Glu	Val	Asn 285	Ser	Leu	Gly
Glu	Arg 290	Tyr	Asp	Phe	Asp	Ser 295	Ile	Met	His	Tyr	Ala 300	Arg	Asn	Thr	Phe
Ser 305	Arg	Gly	Met	Phe	Leu 310	Asp	Thr	Ile	Leu	Pro 315	Ser	Arg	Asp	Asp	Asn 320
Gly	Ile	Arg	Pro	Ala 325	Ile	Gly	Gln	Arg	Thr 330	Arg	Leu	Ser	Lys	Gly 335	Asp
Ile	Ala	Gln	Ala 340	Arg	Lys	Leu	Tyr	Arg 345	Cys	Pro	Ala	Cys	Gly 350	Glu	Thr
Leu	Gln	Glu 355	Ser	Asn	Gly	Asn	Leu 360	Ser	Ser	Pro	Gly	Phe 365	Pro	Asn	Gly
Tyr	Pro 370	Ser	Tyr	Thr	His	Cys 375	Ile	Trp	Arg	Val	Ser 380	Val	Thr	Pro	Gly
Glu 385	Lys	Ile	Val	Leu	Asn 390	Phe	Thr	Thr	Met	Asp 395	Leu	Tyr	Lys	Ser	Ser 400
Leu	Cys	Trp	Tyr	Asp 405	Tyr	Ile	Glu	Val	Arg 410	Asp	Gly	Tyr	Trp	Arg 415	Lys

100-24654

	Ser	Pro	Leu	Leu	Gly	Arg	Phe	Cys	Gly	Asp	Lys	Leu	Pro	Glu	Val	Leu	
			420						425					430			
	Thr	Ser	Thr	Asp	Ser	Arg	Met	Trp	Ile	Glu	Phe	Arg	Ser	Ser	Ser	Asn	
			435					440					445				
5	Trp	Val	Gly	Lys	Gly	Phe	Ala	Ala	Val	Tyr	Glu	Ala	Ile	Cys	Gly	Gly	
		450					455					460					
	Glu	Ile	Arg	Lys	Asn	Glu	Gly	Gln	Ile	Gln	Ser	Pro	Asn	Tyr	Pro	Asp	
	465				470					475					480		
10	Asp	Tyr	Arg	Pro	Met	Lys	Glu	Cys	Val	Trp	Lys	Ile	Thr	Val	Ser	Glu	
				485						490					495		
	Ser	Tyr	His	Val	Gly	Leu	Thr	Phe	Gln	Ser	Phe	Glu	Ile	Glu	Arg	His	
			500					505					510				
	Asp	Asn	Cys	Ala	Tyr	Asp	Tyr	Leu	Glu	Val	Arg	Asp	Gly	Thr	Ser	Glu	
		515						520					525				
5	Asn	Ser	Pro	Leu	Ile	Gly	Arg	Phe	Cys	Gly	Tyr	Asp	Lys	Pro	Glu	Asp	
		530					535					540					
	Ile	Arg	Ser	Thr	Ser	Asn	Thr	Leu	Trp	Met	Lys	Phe	Val	Ser	Asp	Gly	
	545				550					555					560		
20	Thr	Val	Asn	Lys	Ala	Gly	Phe	Ala	Ala	Asn	Phe	Phe	Lys	Glu	Glu	Asp	
				565						570					575		
	Glu	Cys	Ala	Lys	Pro	Asp	Arg	Gly	Gly	Cys	Glu	Gln	Arg	Cys	Leu	Asn	
			580						585					590			
	Thr	Leu	Gly	Ser	Tyr	Gln	Cys	Ala	Cys	Glu	Pro	Gly	Tyr	Glu	Leu	Gly	
		595						600					605				
5	Pro	Asp	Arg	Arg	Ser	Cys	Glu	Ala	Ala	Cys	Gly	Gly	Leu	Leu	Thr	Lys	
		610					615					620					
	Leu	Asn	Gly	Thr	Ile	Thr	Thr	Pro	Gly	Trp	Pro	Lys	Glu	Tyr	Pro	Pro	
	625					630					635					640	
30	Asn	Lys	Asn	Cys	Val	Trp	Gln	Val	Val	Ala	Pro	Thr	Gln	Tyr	Arg	Ile	
				645						650					655		
	Ser	Val	Lys	Phe	Glu	Phe	Phe	Glu	Leu	Glu	Gly	Asn	Glu	Val	Cys	Lys	
			660					665					670				
	Tyr	Asp	Tyr	Val	Glu	Ile	Trp	Ser	Gly	Leu	Ser	Ser	Glu	Ser	Lys	Leu	
		675						680					685				
35	His	Gly	Lys	Phe	Cys	Gly	Ala	Glu	Val	Pro	Glu	Val	Ile	Thr	Ser	Gln	
		690					695					700					
	Phe	Asn	Asn	Met	Arg	Ile	Glu	Phe	Lys	Ser	Asp	Asn	Thr	Val	Ser	Lys	
	705					710					715					720	
40	Lys	Gly	Phe	Lys	Ala	His	Phe	Phe	Ser	Asp	Lys	Asp	Glu	Cys	Ser	Lys	
				725						730					735		
	Asp	Asn	Gly	Gly	Cys	Gln	His	Glu	Cys	Val	Asn	Thr	Met	Gly	Ser	Tyr	
			740					745						750			
	Met	Cys	Gln	Cys	Arg	Asn	Gly	Phe	Val	Leu	His	Asp	Asn	Lys	His	Asp	
		755					760						765				

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Cys Lys Glu Ala Glu Cys Glu Gln Lys Ile His Ser Pro Ser Gly Leu
770 775 780

Ile Thr Ser Pro Asn Trp Pro Asp Lys Tyr Pro Ser Arg Lys Glu Cys
785 790 795 800

5 Thr Trp Glu Ile Ser Ala Thr Pro Gly His Arg Ile Lys Leu Ala Phe
805 810 815

Ser Glu Phe Glu Ile Glu Gln His Gln Glu Cys Ala Tyr Asp His Leu
820 825 830

10 Glu Val Phe Asp Gly Glu Thr Glu Lys Ser Pro Ile Leu Gly Arg Leu
835 840 845

Cys Gly Asn Lys Ile Pro Asp Pro Leu Val Ala Thr Gly Asn Lys Met
850 855 860

Phe Val Arg Phe Val Ser Asp Ala Ser Val Gln Arg Lys Gly Phe Gln
865 870 875 880

5 Ala Thr His Ser Thr Glu Cys Gly Gly Arg Leu Lys Ala Glu Ser Lys
885 890 895

Pro Arg Asp Leu Tyr Ser His Ala Gln Phe Gly Asp Asn Asn Tyr Pro
900 905 910

Gly Gln Val Asp Cys Glu Trp Leu Leu Val Ser Glu Arg Gly Ser Arg
915 920 925

Leu Glu Leu Ser Phe Gln Thr Phe Glu Val Glu Glu Glu Ala Asp Cys
930 935 940

Gly Tyr Asp Tyr Val Glu Leu Phe Asp Gly Leu Asp Ser Thr Ala Val
945 950 955 960

25 Gly Leu Gly Arg Phe Cys Gly Ser Gly Pro Pro Glu Glu Ile Tyr Ser
965 970 975

Ile Gly Asp Ser Val Leu Ile His Phe His Thr Asp Asp Thr Ile Asn
980 985 990

30 Lys Lys Gly Phe His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr
995 1000 1005

Thr His Thr Lys Lys *
1010

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCAGCTTAAC CTGTTACAC

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACCTCTACTT CCACTTCATC

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCAGAACAGA AAGGAATGTG

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACCACTATT CCACATCACC

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTTGCACTC AGTTGCTTTG CTGG

24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAGTGCGGCC GCACATTCCT TTGTGTTC

28

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Tyr Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Glu Thr Met His Ala
1 5 10 15

Lys Asn

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys His Ile Arg Tyr Lys Ser Ile Arg Tyr Pro Asp Thr Thr His Thr
1 5 10 15

Lys Lys